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Mailbox: CM1 8E12 Phone: 703.308.4735

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Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 19B; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-254290/21.
N-PSDB; AAX34759.
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Ehrlichia chaffeen
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E. chafeensis p28
Ehrlichia chaffeen
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Ehrlichia chaffeen
                                                                                                    June 7, 2002, 14:20:58 ; Search time 30.07 Seconds (without alignments) 73:877 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM protein - protein search, using sw model
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) -			287		AAB36182		Cowdria ruminatium
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	· w	20	m	278		AAW51093		Ehrlichia chaffeen
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	28	o.	m	278		AAB36187		Ehrlichia chaffeen
	29	σ.	3	278		AAU04197		variable surface a
	30	σ.	m	280		AAY06945		E. chateensis OMP-
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	32	თ	4	133		AAW51097		canis
	33	o.	4	133		AAB36191		Canis
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KW	Outer	membr		protein;	OMP;	Ehrlichia	chafeensis; E	canis; P30;
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SO	Ehrlichia	chia cani	nis.					
NA PN	W0991	3720-A1	<u> </u>					
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G X	25-MAR	R-1999.						
PF	18-SEP	P-1998;	-	98WO-US19600	.009			
P.R.	19-SE	-SEP-1997;	97U	97US-00593	353.			
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MAP1 homologue; variable surface antigen; VSA4; rickettsla;

Ehrlichia chaffeensis VSA4 protein.

14-SEP-1998 (first entry)

AAW51094;

AAW51094 standard; Protein; 280 AA

AAW51094

Location/Qualifiers

Ehrlichia chaffeensis

DNA vaccine

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Gaps

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The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
       The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -16 to 2) shown.
In AAV06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAV06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                        Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
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                                                                                                                                                 Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           outer membrane proteins from Ehrlichia chaffeensis and
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                                                                                                                                                 Score 110; DB 20;
Pred. No. 1.5e-09;
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                                                                                                                                                                                                                                                                                                          AAY06948 standard; Protein; 280 AA.
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                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                        60 ntttgvfglkgdwdgatikd 79
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                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OHIS ) UNIV OHIO STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shrlichia chafeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-254290/21.
N-PSDB; AAX34748.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 AA;
                                                                                                            288 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shrlichia, canis
                                                                                                                                                                                                                                                                                                                                                                                                                                           detection; dog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9913720-A1.
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                                                                                                             Sequence.
                                                                                                                                                                                                                                                                                                                                        AAY06948;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Composition costaining nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                             Ganta RR, Mahan SM, McGuire TC;
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                                                                                                                                                                   /note- "putative signal peptide"
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Pred. No. 2.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 2B; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%;
88.9%;
                                                                                                                                                                                                                                                   97WO-US19044
                                                                                                                                                                                                                                                                               96US-0733230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barbet AF, Burridge MJ,
Nyika A, Rurangirwa FR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                         (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-251232/22.
N-PSDB; AAV07179.
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nes 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 AA;
                                                                                                                                                                                              W09816554-A1
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                                                                                                                                                                                                                           23-APR-1998.
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                                                                                                                                                         Peptide
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Matches
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ID AAB3
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Gaps

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Length 280; Indels

DB 20;

Score 96;

87,3%;

Query Match 87.3%; Best Local Similarity 94.4%; Matches 17; Conservative

1 NTTTGVFGLKQDWDGATI 18

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Pred. No. 2.5e-07; 1; Mismatches 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAPI) of Ehrlichia sp. The MAPI gene may be used in a vaccines to protect animals or humans against rickettsial dispass caused by a organisms of Rickettsial sp. Ehrlichia sp. Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines can be driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria runnhaulum genes designated map 2, Ihworf3, 4hworf1, 18hworf1 and against designated map 2, Ihworf3, 4hworf1, 18hworf1 and are used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                           McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                   najor antigenic protein 1; antirickettsial; vaccine; gene therapy;
Rickettsia; Cowdria; Anaplasma; map2; lhworf3; 4hworf1; 18hworf1;
                                                                                                                                                                                                                                                                                                                                                                                         Mahan SM, McGuire
re WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Major antigenic protein; MAP; vaccine; immunogenic; rickettsia;
infection; heartwater; diagnostic; variable surface antigen; VSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels '0;
                                                                                                 Shrlichia chaffeensis; VSA4; variable surface antigen 4; MAP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Variable surface antigen 4 (VSA4) from Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%; Score 90; DB 21; Length 280; 88.9%; Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                         Ganta RR, Burridge MJ, Mahan nd AL, Simbl BH, Whitmire WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU04198 standard; Protein; 280 AA.
                                                                  Ehrlichia chaffeensis partial VSA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 45-46; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                         Barbet AF, Bowle.MV, Ganta
Rurangirwa FR, Moreland AL,
                                                                                                                                                                                                                                                                                     21-APR-2000; 2000WO-US10886.
                                                                                                                                                                                                                                                                                                                      99US-0130725.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                    (first entry)
                                                                                                                                                                                   Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                        (UYFL ) UNIV FLORIDA.
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Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-679675/66.
N.PSDB; AAC68705.
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AAB36188;
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The sequence represents the amino acid sequence of variable surface antigen 4 (VSA4) isolated from Ehrlichia chaffeensis, which as similarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious
                                                                                                                                                                                                                                                                                   New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30; detection; dog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                           Barbet AF, Ganta RR, McGuire TC, Burridge MJ, Rurangirwa FR, Mahan SM, Bowie MV, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 90; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 2.3e-06; ; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 2A-2B; 30pp; English
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88.9%;
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                                                                                                                                   96US-0733230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NTTTGVFGLKQDWDGATI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E. chafeensis p28 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 88.9°
Matches 16; Conservative
            Ehrlichia chaffeensis
                                                                                                                                                                 (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ehrlichia chafeensis,
                                                                                                                                                                                                                                           WPI; 2001-424487/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 AA;
                                                                                                                                                                                                                                                           N-PSDB; AAS07578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9913720-A1.
                                                                                                      17-OCT-1997;
                                                                                                                                   .7-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-SEP-1998;
                                         US6251872-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1999.
                                                                      26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY06942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY06942
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97US-0059353

19-SEP-1997;

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Ehrlichla chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1. -1(B to Z) shown in AAVG0943-958. The E. cânis proteins form part of the P30 family and consist of proteins shown in AAVG0959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition containing nucleic acid encoding rickettsial antigen useful for, e.g. stimulating protective immune response in humans or
                                                                                                                                                                            The invention provides isolated outer membrane proteins (OMP) from
                                                                                                        Novel outer membrane proteins from Ehrlichia chaffeensis and Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP1 homologue; variable surface antigen; VSA5; rickettsia;
                                                                                                                                                                                                                                                                                                     Query Match 74.5%; Score 82; DB 20; Length 256; Best Local Similarity 70.0%; Pred. No. 4e-05; Matches 14; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlichia chaffeensis VSA5 protein (partial sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note- "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mahan SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ganta RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW51095 standard; Protein; 276 AA.
                                                                                                                                                   Claim 18; Fig 1; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                    3 nttvgvfglkqnwdgsalsn 53
                                                                                                                                                                                                                                                                                                                                                         1 NTTIGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0733230.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        · 97WO-US19044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barbet AF, Burridge MJ, Nyika A, Rurangirwa FR;
                      (OHIS ) UNIV OHIO STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-251232/22.
                                            Ohashi'N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ehrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UYFL ) UNIV FLORIDA
                                                                       WPI; 1999-254290/21
                                                                                                                                                                                                                                                                   256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV07179
                                                                                    N-PSDB; AAX34742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-0CT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09816554-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ONA vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW51095;
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW51095
ID AAW5
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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McGuire TC;

Claim 3; Fig 2B; 39pp; English.

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animals

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This is the near full-length variable surface antigen VSA5 protein of Ehrlichia chaffeensis; it lacks about 5-7 C-terminal amino acid residues. The VSA5 amino acid sequence was deduced from a partial open reading frame (ORF5) of a genomic locus (see AAV07179) of E. chaffeensis that was obtained on the basis of homology to the major antigenic protein MAPI (see AAM51088) of Cowdria rundinantium. This genomic locus included 5 ORFs encoding similar, but non-identical proteins (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW51091-95). A claimed composition comprises a nucleic acid (see AAW51091-95). In muna or veterinary medicine. In vaccines to protect against Rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia. Ehrlichia, anaplasma and Cowdria species. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McGuire TC;
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence shows a high degree of similarity to the major antigenic protein 1 (MAP1) of Ehrlichia sp. The MAP1 gene may be used in a vaccines to protect animals or humans against rickettsial diseases caused by a organisms of Rickettsia sp., Ehrlichia sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ganta RR, Burridge MJ, Mahan SM, McGuire nd AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrlichia chaffeensis, VSA5, variable surface antigen 5, MAP1, major antigenic protein 1, antirickettsial; vaccine, gene therapy, Rickettsia, Cowdria, Anaplasma, map2, 1hworf3, 4hworf1; 18hworf1;
                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                     Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                     Score 82; DB 19;
Pred, No. 4.3e-05;
3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ehrlichia chaffeensis partial VSA5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB36189 standard; Protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Page 47; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barbet AF, Bowle MV, Ganta
Rurangirwa FR, Moreland AL,
                                                                                                                                                                                                                                                                                                                                                                     74.5%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-APR-2000; 2000WO-US10886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0130725
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 70.0%
Matches 14; Conservative·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYFL.) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-679675/66.
N-PSDB; AAC68706.
                                                                                                                                                                                                                                                                                                                   276 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W0200065063-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-NOV-2000
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3gdorf3.
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Gaps

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276 AA;

Sequence

us-10-054-647-2.rag

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Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettsial pathogen. The nucleic acid vaccines defivien by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria ruminatium genes designated map 2, Ihworf3, 4hworf1, 18hworf1 and 3gdorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                      Length 276;
                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                   74.5%; Score 82; DB 21;
70.0%; Pred. No. 4.3e-05;
tive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                         1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                     59 nttvgvfglkgnwdgsaisn 78
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                     276 AA;
                                                                                                                                                                                                     Sequence
8888888888
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AAU04199 standard; Protein; 276 AA (first entry) 23-OCT-2001 AAU04199,

Variable surface antigen 5 (VSA5) from Ehrlichia chaffeensis.

Major antigenic protein; MAP; vaccine; immunogenic; rickettsia; infection; heartwater; diagnostic; variable surface antigen; VSA

Ehrlichia chaffeensis

JS6251872-B1

Ganta RR, Mahan SM, McGuire TC;

Barbet AE, Burridge MJ, Nyika A, Rurangirwa FR;

WPI; 1998-251232/22. N-PSDB; AAV07177.

(UYFL) UNIV FLORIDA.

26-JUN-2001.

97US-0953326 17 cocr-1997;

96US-0733230. 17-0CT-1996;

(UYEL) UNIV FLORIDA

Nyika A; McGuire TC, Burridge MJ, SM, Bowie MV, Alleman AR; Barbet AF, Ganta RR, McG Rurangirwa FR, Mahan SM,

WPI; 2001-424487/45. N-PSDB; AAS07578 New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures

Example 3; Fig 2A-2B; 30pp; English.

The sequence represents the amino acid sequence of variable surface antigen 5 (VSA5) isolated from Ehrlichia chaffeensis, which has similarity to major antigen protein (MAP). The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to traise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is

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Gaps
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                                                                                                                    MAP1 gene; major antigenic protein 1; rickettsia; DNA vaccine.
Length 276;
             3; Indels
                                                                                                        Ehrlichia chaffeensis major antigenic protein 1 (MAP1).
Score 82; DB 22;
Pred. No. 4.3e-05;
3; Mismatches 3;
                                                                    AAW51089 standard; Protein; 280 AA,
                                                                                                                                                                     97WO-US19044.
 74.5%;
70.0%;
                         20
                                96US-0733230
                                                                                            (first entry)
                         1 NTTTGVFGLKQDWDGATIKD
Query Match 74.5
Best Local Similarity 70.0
Matches 14; Conservative
                                                                                                                                Ehrlichia chaffeensis
                                                                                                                                             WO9816554-A1.
                                                                                            14-SEP-1998
                                                                                                                                                         23-APR-1998.
                                                                                                                                                                     17-OCT-1997;
                                                                                                                                                                                 17-0CT-1996;
                                                                               AAW51089;
                                                              AAW51089
                                                        RESULT
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ANOUNTICE A Claimed Composition comprises a nucleic acid (see AANONNTO-16-82) encoding a polypeptide (see AANONNTO-16-82) encoding a polypeptide (see AANONTO-16-82) encoding a polypeptide (see AANONTO-16-82) encoding a polypeptide (see AANONTO-16-82) interestories against the response against a rickettsial pathogen. The nucleic acid is used, in human or veterinary medicine, in vaccines to protect against Rickettsia. Bhiliohia, Anaplasma and Cowdria remains episomal and capable of expressing polypeptide for at least 19 mth. The Ehrlichia antigenic polypeptides can be used diagnostically to detect antibodies associated with Ehrlichia infection (claimed). Composition containing nucleic acid encoding rickettsial antigen - useful for, e.g. stimulating protective immune response in humans or animals This polypeptide comprises the major antigen protein 1 gene (MAP1) Claim 3; Page 18-19; 39pp; English

280 AA; Sequence

Gaps ö Length 280; 74.5%; Score 82; DB 19; Length 28 70.0%; Pred. No. 4.4e-05; 1ve 3; Mismatches 3; Indels Best_Local Similarity 70.0% Matches 14; Conservative Query Match

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1 NTTTGVFGLKQDWDGATIKD 20 8 g

60 nttvgvfglkqnwdgsaisn 79

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New MAP2 genes and polypeptides useful as vaccines for conferring immunity to human and animal rickettsial diseases, e.g. heartwater, or as molecular markers in nucleic acid analysis procedures
                           antigenic protein 1; MAP1; vaccine; immunogenic; rickettsia;
Major antigenic protein 1 (MAPI) from Ehrlichia chaffeensis.
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 15-17; 30pp; English
                                             infection; heartwater; diagnostic.
                                                                                                                                                                                                                                                   Barbet AF, Ganta RR, Mc(
Rurangirwa FR, Mahan SM,
                                                                       Ehrlichia chaffeensis
                                                                                                                                                                                                                      (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                            WPI; 2001-424487/45.
N-PSDB; AAS07576.
                                                                                                                                                             .7-OCT-1997;
                                                                                                                                                                                          17-0CT-1996;
                                                                                                    US6251872-B1
                                                                                                                                 26-JUN-2001.
                                 Ma jor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY06943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is given in a specification relating to nucleic acid vaccines containing genes to protect animals or humans against rickettaial diseases caused by a organisms of Rickettaia sp., Ehrlichia sp., Anaplasma sp. or Cowdria sp. The vaccine elicits an immune response protective against the rickettaial pathogen. The vaccine comprises the major antigenic protein 1 (MAPI) gene or the major antigenic protein 2 (MAP2) gene of rickettsial pathogens. The nucleic acid vaccines can be
                                                                                                                                                 Ehrlichia chaffeensis; MAP1; major antigenic protein 1; antirickettsial;
vaccine; gene therapy; Rickettsia; Cowdria; Anaplasma; map2; 1hworf3;
4hworf1; 18hworf1; 3gdorf3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides useful as DNA vaccines for conferring immunity to rickettsial infection e.g. heartwater caused by Cowdria ruminantium, comprises major antigenic protein 1 or 2 gene of rickettsial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 driven by the human cytomegalovirus (HCMV) enhancer-promoter. Cowdria ruminatium genes designated map 2, 1hworf3, 4hworf1, 18hworf1 and 39dorf3 may be used in therapeutic and diagnostic applications. The polypeptides are useful for detecting antibodies associated with infection by a rickettsial pathogen whilst the polynucleotides may be used to detect the presence of rickettsial nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                      McGuire
                                                                                                                                                                                                                                                                                                                                                                                      Ganta RR, Burridge MJ, Mahan SM, McGuire
nd AL, Simbi BH, Whitmire WW, Alleman AR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74.5%; Score 82; DB 21; 70.0%; Pred. No. 4.4e-05; Live 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 35-36; 63pp; English.
                                 AAB36183 standard; Protein; 280 AA.
                                                                                                                                                                                                                                                                                                                                                                                      Barbet AF, Bowie MV, Ganta
Rurangirwa FR, Moreland AL,
                                                                                                                                                                                                                                                                                                 11-APR-2000; 2000WO-US10886.
                                                                                                                                                                                                                                                                                                                            99US-0130725.
                                                                                                                       Ehrlichia chaffeensis MAP1
                                                                                                                                                                                                           Shrlichia chaffeensis
                                                                                                                                                                                                                                                                                                                                                         (UYEL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-679675/66.
N-PSDB; AAC68700.
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Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 AA;
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                                                                                          02-MAR-2001
                                                                                                                                                                                                                                                                   02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                              AAB36183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
       RESULT 11
                     AAB36183
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Nyika A;

Burridge MJ, , Alleman AR;

McGuire TC, Bu SM, Bowie MV,

96US-0733230 97US-0953326

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The sequence represents the amino acid sequence of major antigenic protein 1 (MAP1) from Ehrlichia chaffeensis. The MAP polynucleotides and polypeptides are useful as vaccines for conferring immunity to rickettsia infection, including Cowdria ruminantium causing heartwater. The MAP polynucleotides may be used as molecular markers in nucleic acid analysis procedures, and to produce the MAP polypeptides, which may be used to raise antibodies that are reactive with the polypeptides. The nucleic acids may further be used as probes to identify complementary sequences within other nucleic acid molecules or genomes, where such probes can be applied to identify or distinguish infectious strains of organisms in diagnostic procedures or in rickettsial research where identification of particular organisms or strains is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 82; DB 22; Length 280;
Pred. No. 4.4e-05;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY06943 standard; Protein; 281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           74.5%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 nttvgvfglkqnwdgsaisn 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. chafeensis OMP-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 NTTTGVFGLKQDWDGATIKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ehrlichia chafeensis
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection; dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09913720-A1
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                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
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Gaps

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Indels

1 NTTTGVFGLKQDWDGATIKD 20

Conservative

AAU04193 standard; Protein; 280 AA.

RESULT 12

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(flust entry)

23-OCT-2001

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AAU04193

AAU04193 ID AAU0. XX AC AAU0. XX DT 23-0

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of the OMP family and consist of proteins OMP-1, -1(B to 2) shown in AAY06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAY06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                        280 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehrlichia canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200032745-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-1998;
03-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-NOV-1999;
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                                                                                                                                                                                                                                                                                                 AAY71479;
                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
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                                                                                                                                                                                                                                        The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAVG6943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAVG6959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Outer membrane protein; OMP; Ehrlichia chafeensis; E. canis; P30;
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                      outer membrane proteins from Ehrlichia chaffeensis and
                                                                                                                                                                                                                                                                                                                                                                                    Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                    74.5%; Score 82; DB 20; L. 70.0%; Pred. No. 4.4e-05; iive 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY06962 standard; Protein; 280 AA.
                                                                                                                                                                                                                 Disclosure; Fig 3B; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US19600.
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              98WO-US19600
                                            97US-0059353
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                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 70.0
nes 14; Conservative
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                                                                       (OHIS ) UNIV OHIO STATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohashi N, Rikihisa Y;
                                                                                                 Ohashi N, Rikihisa Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-254290/21.
N-PSDB; AAX34762.
                                                                                                                              API; 1999-254290/21
                                                                                                                                         N-PSDB; AAX34743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ehrlichia canis
                                                                                                                                                                                   Ehrlichia canis
                                                                                                                                                                                                                                                                                                                                          281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection; dog
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              18-SEP-1998;
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                                            19-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
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The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part

Novel outer membrane proteins from Ehrlichia chaffeensis and

Disclosure, Fig. 22B; 55pp; English.

Ehrlichia canis

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The patent relates to homologous 28-kiloDalton (kDa) protein genes of Ehrlichia canis, designated ECa28SA1, ECa28SA2, ECa28SA3, ECa28-1 and ECa28-2. These genes are members of a polymorphic multiple gene family and contained in a single locus of 5.592 kb. The 28-kDa proteins are immunoreactive with anti-E. canis serum hence are important immunoprotective antigens. The protein is useful for vaccinating against E. canis infections such as canine ehrlichiosis in dogs.
                                                                                                                                                                                                                                                                                                                             Homologous 28-kDa protein gene; ECa28SA3; immunoreactive; vaccine; p28 gene; p01% gene; p01, multiple gene family; immunoprotective antigen; antibacterial; canine ehrlichiosis; canine tropical pancytopaenia; tick-borne rickettsial disease; serodiagnosis.
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Canine ehrlichiosis, also known as canine tropical pancytopaenia, is tick-borne rickettsial disease of dogs. Eca28-1 is conserved amongst different strains of E. canis and hence useful for serodiagnosis of canine ehrlichiosis. The present sequence is a E. canis ECa28SA3 30-kDa protein which is post-translationally modified to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ehrlichia canis antigens useful for vaccinating against canine ehrlichiosis in dogs
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                  Length 280
                                                 4; Indels
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/label- Mature_ECa28SA3_28-kDa_protein
                                                                                                                                                                                                                                                                                               Ehrlichia canis immunoreactive protein ECa28SA3
                 Score 77; DB 20;
Pred. No. 0.00028;
3; Mismatches 4.
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/label- Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualiflers
                                                                                                                                                                                               AAY71479 standard; Protein; 280 AA.
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                  70.0%;
                                                                                  1 NTTTGVFGLKQDWDGATIKD 20
                                                                                                   1:| |||||| ||:| || :
59 nstvqvfqlkhdwnggtisn 78
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Query Match
Best Local Similarity 65.00,
-hos 13, Conservative
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99US-0261358
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N-PSDB; AAD01294, AAD01295.
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mature 28-kDa protein by cleavage of N-terminal signal sequence. ပ္တန္တင္တ

Sequence 280 AA;

0; Gaps Query Match
Best Local Similarity 65.0%; Pred. No. 0.00028;
Matches 13; Conservative 3; Mismatches 4; Indels

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1 NTTTGVFGLKQDWDGATIKD 20 |:| |||||| ||:| ||: 59 nstvgvfglkhdwnggtign 78

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Search completed: June 7, 2002, 14:30:16 Job time: 558 sec

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Query Match
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Matches
                                                                                 June 7, 2002, 14:27:08 ; Search time 13.08 Seconds (without alignments) 37.348 Million cell updates/sec
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                               lotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS-08-828-741B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-268-347-48
                                                                                                                                                                                                                                                    231628 segs, 24425594 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
                                                                                                                                              US-10-054-647-2
110
1 NTTTGVFGLKQDWDGATIKD 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length; 200000000
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Match Length
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Perfect score:
Sequence:
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ALIGNMENTS

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APPLICANT: SCULTA APPLICANT: McDael APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Burridge, Michael J.
APPLICANT: Mahan, Suman M.
ITITE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of TITE OF INVENTION: Animals and Humans
FILE REFERENCE: UP-16701
CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT APPLICATION NUMBER: 08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,330
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NOS: 24
SCO ID NO 17
SED ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Sequence 17, Application US/08953326 Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT:
CRGANISM: Ehrlichia chaffeensis
US-08-953-326-17
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88.9%;
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les 16; Conservative
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RESULT 2
US-08-953-326-18
Sequence 18, Application US/08953326
Sequence 18, Application US/08953326
GENERAL INFORMATION:
APPLICANT: Barbet, Anthony F.
APPLICANT: Ganta, Roman R.
APPLICANT: Mcduire, Travis C.
APPLICANT: Buridge, Michael J.
APPLICANT: Buridge, Aceme
APPLICANT: Nylka, Aceme
APPLICANT: Rurangirwa, Fred R.

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Patentin Ver. 2.0
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APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Nucleic Acid Vaccines Against

Rickettsial Diseases and Methods of Use
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                                                                                                                                                                                                                                                                                                                                                                                                                     uvery match 74.5%; Score 82; DB 4;
Best Local Similarity 70.0%; Pred. No. 9.5e-06;
Matches 14; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                     CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1996-10-17
NUMBER: OF SEQ. ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 276
TYPE: PAT
US-08-953-326-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/733,230
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Ganta, Roman Reddy
McGuire, Travis C.
Burridge, Michael J.
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ATTORNEY/AGENT INFORMATION:
NAME: WHILLOCK, Ted W.
RESISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: P
TITLE OF INVENTION: B
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mahan, Suman M.
TITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
TITLE OF INVENTION: Animals and Humans
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Length 280;
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Pred. No. 9.6e-06;
Ouery Match 74.5%; Score 82; DB Best Local Similarity 70.0%; Pred. No. 9.6e Matches 14; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Mismatches
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CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-1017
EARLIER APPLICATION NUMBER: 08/733,230
EARLIER FILING DATE: 1996-10-17
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CURRENT FILING DATE: 1997-10-17
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EARLIER FILING DATE: 1997-10-17
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Patent No. 6251872
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08953326 Patent No. 6251872
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US-08-953-326-4
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 280
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                                                                                                           1 NTTTGVFGLKQDWDGATIKD 20
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Best Local Similarity 70.0%;
Matches 14; Conservative
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IIILE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of IIILE OF INVENTION: Animals and Humans
                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER APPLICATION NUMBER: 08/733,230
EARLIER FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 24
SOCTWARE: Patentin Ver. 2.0
SEQ ID NO 2:
LENGTH: 287
                   Sequence 2, Application US/08953326
Patent No. 6251872
                                                                               APPLICANT: Barbet, Anthony F. APPLICANT: GATLEA, ROMAIN R. APPLICANT: McGulre, Travis C. APPLICANT: Burridge, Michael J. APPLICANT: Nyika, Aceme APPLICANT: Ruiangliwa, Fred R. APPLICANT: Mahan, Suman M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Cowdria ruminantium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 54.1
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 NTQT-VFGLKKDWDG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 NTTTGVFGLKODWDG 15
                                                                                                                                                                                                                                                                       FILE REFERENCE: UF-167C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-953-326-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Nucleic Acid Vaccines Against
TITLE OF INVENTION: Rickettsial Diseases and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59.5; DB 3; Length 287; Pred. No. 0.043;
                                                                                                                                              Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                       4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
JURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/733,230
                                                                                                                                          64.5%; Score 71; DB 4; 66.7%; Pred. No. 0.00059; 1ve 2; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Sallwanchik & Sallwanchik
: 2421 N.W. 41st Street, Suite A-1
Galnesville
                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08733230 Patent No. 6025338 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF-16
TELECOMMUTICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burridge, Michael J.
Nyika, Aceme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rurangirwa, Fred R.
Mahan, Suman M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SISTEM: PC-DOS/MS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Barbet, Anthony F.
Ganta, Roman Reddy
McGuire, Travis C.
                                                     ORGANISM: Ehrlichia chaffeensis US-08-953-326-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.1%;
80.0%;
                                                                                                                                                                                                                                                 60 NTTVGVFGIEODWDRCVI 77
                                                                                                                                                                                                                              1 NTTTGVFGLKQDWDGATI 18
                                                                                                                                            Query Match
Best Local Similarity 66.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 54.1
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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SEQ ID NO 15
LENGIH: 28
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Gaps

1; Indels

1; Mismatches

Length 287;

5; DB 4 0.043;

Score 59.5; Pred. No. 0

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PPLICANT: Mahan, Suman M.
ITLE OF INVENTION: Nucleic Acid Vaccines Against Rickettsial Diseases of
ITLE OF INVENTION: Animals and Humans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59; DB 4
Pred. No. 0.05
3; Mismatches
                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER APPLICATION WUMBER: 08/733,230
EARLIER FILING DATE: 1996-10-17
Sequence 16, Application US/08953326 Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Ehrlichia chaffeensis
US-08-953-326-16
                                                                                                                                                                                    APPLICANT: Rurangirwa, Fred R. APPLICANT: Mahan, Suman M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.6%;
                                                                                                                                         APPLICANT: Burridge, Michael J
                                                                      APPLICANT: Barbet, Anthony F. APPLICANT: Ganta, Roman R.
                                                                                                             APPLICANT: McGuire, Travis C
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 9; Conserval
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1 NTTTGVFGLKQDWDG 15

1 NTTTGVFGLKQDWDG 15

RESULT

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Sequence 2, Application US/08991942
Patent No. 6015673
GENERAL INFORMATION:
APPLICANT: GONZALEZ, Frank J.
APPLICANT: GONZALEZ, Frank J.
APPLICANT: FERRANDEZ-SALGHERO, PEGTO
APPLICANT: FERRANDEZ-SALGHERO, PEGTO
APPLICANT: FERRANDEZ-SALGHERO, PEGTO
APPLICANT:
APPLICANT: FERRANDEZ-SALGHERO, PEGTO
TITLE OF INVENTION: DIMPROPYRIMIDINE DEHYDROGENASE
NUMBER OF SEQUENCES: 13
CORRESSONDENCES ADDRESSE:
ADDRESSEE: TOWNSEND and TOWNSEND Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                          36.8%; Score 40.5; DB 2; Length 1025; 42.9%; Pred. No. 2.2e+02; tive 2; Mismatches 7; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/991,942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
36.8%; Score 40.5; DB 3;
Best Local Similarity, 42.9%; Pred. No. 2.2e+02;
Matches 9; Conservative 2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/304,309
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 15280-210
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               736 NTVSGLMGLKSDGTPWPAVGI 756
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                       1 NITIGVEGLKOD---WDGATI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 543-9600
(415) 543-5043
                                                                                                           1025 amino acids
                                          (415) 543-5043
R SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              36.8%
Query Match
Best Local Similarity 42.9%
Matches 9; Conservative
                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-991-942-2
                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-304-309-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     California
                                                                                                                  TOPOLOGY: 11nc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                            INFORMATION FOR
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US-08-991-942-2
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                                                                                                         LENGIH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: CLONING AND EXPRESSION OF CDNA FOR HUMAN TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
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Pred. No. 0.89;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION WINBER: US/08/953,326
CURRENT FILING DATE: 1997-10-17
EARLIER APPLICATION NUMBER: 08/953,326
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1997-10-17
EARLIER FILING DATE: 1996-10-17
NUMBER OF SEQ ID NÖS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: SMICH, TAMOGHY L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 15280-210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JMBER: US/08/304,309
09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                              Sequence 20, Application US/08953326
Patent No. 6251872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08304309
Patent No. 5856454
GENERAL INFORMATION
APPLICANT: GONZALEZ, Frank J.
APPLICANT: FERNANDEZ-SALGUERO, F.
                                                                                                                                                                                                                                            APPLICANT: McGuire, Travis C. APPLICANT: Burridge, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.5%;
                                                                                                                                                                                                                                                                                           PLICANT: Nyika, Aceme
PLICANT: Rurangirwa, Fred R.
                                                                                                                                                                                                  APPLICANT: Barbet, Anthony F. APPLICANT: Ganta, Roman R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , TYPE; PRT
, ORGANISM: Ehrlichia canis
US-08-953-326-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TTGVFGLKQDWDGATI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 TTVVYGLKENWAGDAI.77
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                       60 NPTVALYGLKQDWEG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94105-1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                             JS-08-953-326-20
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US-08-304-309-2
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Gaps Length 1025; Indels

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4; Mismatches
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CURRENT FILING DATE: 1999-03-16
NUMBER OF SEQ ID NOS: 54.
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           686 TVTFGLSQDSGLTIGKSTLNNDGLTVKD 713
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 48, Application US/09268347
Patent No. 6335182
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09550338 Patent No. 6210951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-268-347-48
                                                                                                                                                                                                                                                      736 NTVSGLMGLKSDGTPWPAVGI 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                              1 NTTTGVFGLKQD---WDGATI 18
1025 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KAWASAKI, Hisashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 TGVFGLKQDWDGATIKD 20
                                                        MOLECULE TYPE: protein
                     amino acid
                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 48
LENGTH: 2048
                                                                              PCT-US95-04567-4
                                                                                                                                                                                                                                                                                                                                                     JS-09-268-347-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-550-338-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-550-338-2
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                         TITLE OF INVENTION: Immunological Materials and Methods for Detecting TITLE OF INVENTION: Dihydropyrimidine Dehydrogenase FILE REFERENCE: 09/138,103 Yoshikubo, et al. CURRENT APPLICATION NUMBER: US/09/138,103A CURRENT FILING DATE: 1998-08-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE NUMBER OF SEQUENCES: 28 CORRESPONDENCE ADDRESS: ADDRESSE: ALDOLD, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: IBM PC COMPOTEDIE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: WILSON, MARK B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: UOAB025P--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04567
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 97114630.3
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 2
LENGTH: 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,357
FILING DATE: 13-APR-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application PC/TUS9504567
GENERAL INFORMATION:
APPLICANT:
                                                                            Sequence 2, Application US/09138103A Patent No. 6232448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               736 NIVSGLMGLKSDGTPWPAVGI 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 NTTTGVFGLKQD---WDGATI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.8%;
nilarity 42.9%;
Conservative
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(713) 789-2679
                                                                                                                                           APPLICANT: Yoshikubo, Takashi
APPLICANT: Hasegawa, Masami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT; ORGANISM: Homo sapiens US-09-138-103-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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APPLICANT: LOOSMOTE, Sheena M.
TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
FILE REFERENCE: 1038-860
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APPLICANT: WIARRA, Yoshihiro
APPLICANT: MIARRA, Yoshihiro
APPLICANT: MIARRA, Yoshihiro
APPLICANT: MIARRA, Yoshihiro
APPLICANT: MIARRA, Yoshihiro
APPLICANTON: GMP Synthetase and Gene Coding for the Same
FILE REFERENCE: 0010-1101-0
CURRENT APPLICATION NUMBER: US/09/550,338
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: JP 11-114787
PRIOR FILING DATE: 1999-04-22
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Ouery Match 36.8%; Score 40.5; DB 5; Length 1025; Best Local Similarity 42.9%; Pred. No. 2.2e+02; Matches 9; Conservative 2; Mismatches 7; Indels 3
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Search completed: June, 7, 2002, 14:30:3 Job time: 208 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw.model

June 7, 2002, 14:27:58; Search time 15.01 Seconds Run on:

US-10-054-647-2 Title: Perfect score:

110 .1 NTTTGVFGLKQDWDGATIKD 20 sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 segs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	probable leucyl am	hypothetical prote	Na+/K+-exchanging	hypothetical prote	rhizobiocin/RTX to	probable phosphoes	conserved hypothet	hypothetical prote	hypothetical prote	probable formate a	probable activatin	probable activatin	hypothetical prote	S-adenosylmethioni	conserved hypothet	dnaA protein - Str	-
	G75483	G87276	A56594	C86822	AH3098	A96188	AE0293	AI2476	C72390	S56603	A91296	D86137	T44893	F75379	T08297	A41870	-
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	43	43	43	43	43	. 43	42.5	42	42.	42	42	42	42	42	42	. 42	•
	30	31	32	33	34	35	36	37	38	. 39	40	41	42	7.43	44	45	

ALIGNMENTS

28k surface antigen 4 - Ehrlichia chaffensis

C; Species: Ehrlichia chaffensis

C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999 C;Accession: JE0217

R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R. Blochem. Blophys. Res. Commun. 247, 636-643, 1998 A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tril A;Reference number: JE0216; MUID:98321180 A;Accession: JE0217

A; Molecule type: DNA A; Residues: 1-280 <RED> A; Cross-references: GB: AF062761

Gaps Score 90; DB 2; Length 280; Pred. No. 1.8e-06; 1; Mismatches 81.8%; 88.9%; Conservative Query Match Best Local Similarity Matches 16; Conserv

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RESULT JE0218

28k surface antigen 5 - Ehrlichia chaffensis

N;Alternate names: MAP1 C;Species: Ehrlichia chaffensis C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999

C; Accession: JE0218
R; Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R. Bartenem Biophys. Res. Commun. 247, 636-643, 1998
Biochem Biophys. Res. Commun. 247, 636-643, 1998
A; Tetle: Molecular characterization of a 28kDa surface antigen gene family of the tri A; Reference number: JE0216; MUID: 98321180

A; Molecule type: DNA

A; Residues: 1-276 <RED>
A; Cross-references: GB: AF062761

Gaps Length 276; Ouery Match 74.5%; Score 82; DB 2; Length 276 Best Local Similarity 70.0%; Pred. No. 3.1e-05; Matches 14; Conservative 3; Mismatches 3; Indels

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1 NTTTGVFGLKQDWDGATIKD 20 ŏ ద

- Ehrlichia chaffensis

28k surface antigen 2 - V;Alternate names: MAP1

Accession: JE0219

Score 71; DB 2; Length 286; Pred: No. 0.0017;

4; Indels

2; Mismatches

Query Match
Best Local Similarity 66.7%;
Matches 12; Conservative

A; Cross-references: GB: AF062761

A; Molecule type: DNA A; Residues: 1-286 <RED>

A; Accession: JE0219

1 NTTTGVFGLKQDWDGATI 18 : 60 NTTVGVFGIEQDWDRCVI 77

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28k surface antigen 3 - Ehrlichia chaffensis

N; Alternate names: MAP1

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hypothetical protein ECs0542 [Imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 (Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 (Straysshi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res 8, 11-22, 2001 #Jul-2001 #Jul-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: B85547
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Latre, 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable RTX family exoprotein [imported] - Escherichia coli (strain 0157:H7, substra C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb;2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Čross-references: GB:AE005174; NID:q12513368; PIDN:AAG54838.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain 0157:H7, substrain EDL933
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A;Cross-references: GB:BA000007; PIDN:BAB33965.1; PID:913360000; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetios:
A;Gene: ECs0542
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bumetanide-sensitive Na-K-Cl cotransporter - spiny dogfish
C;Species: Squalus acanthias (spiny dogfish)
C;Date: O2-Jun-1994 #sequence_revision O2-Jun-1994 #text_change O2-Mar-2001
C;Accession: A53491
     Gaps
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Pred. No. 37;
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illarity 60.0%;
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Best Local Similarity 60.0
Matches 9; Conservative
     10; Conservative
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R;Reddy, G.R.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R.
Bicchem, Blophys. Res. Commun. 247, 636-643, 1998
A;Itle: Molecular characterization of a 28kDa surface antigen gene family of the tribe A;Reference number: JE0216; MUID:98321180
A;Accession: JE0216
                                                                                                                                                                                                                                                                                                                                                            Fireddy, Cr.; Sulsona, C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R. Bicchem. Biophys. Res. Commun. 247, 636-643, 1998
A;Title: Molecular characterization of a 28kDa surface antigen gene family of the tribe A;Reference number: JE0216; MUID:98321180
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C; Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
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C;Species: Cowdria ruminantium (heartwater rickettsia)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
                                                                                                                                                                                                                   C:Species: Ehrlichia chaffensis
C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 17-Mar-1999
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Length 278; Indels

53.6%; Score 59; DB 2 60.0%; Pred. No. 0.12;

Ouery Match 53.6
Best Local Similarity 60.0
Matches 9; Conservative

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A;Cross-references: GB:AF062761

A; Residues: 1-278 <RED> A; Molecule type: DNA

A; Status: preliminary; translated from GB/EMBL/DDBJ

Molecule type: DNA

Residues: Genetics: 53.6%;

Query Match Best Local Similarity

2; Mismatches

: ογ

46.4%;

Local Similarity 58.8 nes 10; Conservative

Matches

Query Match

8k surface antigen 2 - Ehrlichia canis

us-10-054-647-2.rpr

A; Accession: A53491

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Cross-references: EMBL:249704; NID:9825540; PIDN:CAA89777.1; PID:9825545; GSPDB:GNO Experimental source: strain AB972
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J. Bacteriol. 175, 5395-5402, 1993
Akititle: Comparative analysis of flagellin sequences from Escherichia coli strains po
Akeference number: A48658; MUID:93374833
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C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 26-Aug-1999
                                                                                                                                                                                              C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
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C;Superfamily: flagellin
                                                                                                 N;Alternate names: hypothetical protein YM8021.05c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jii1-100c accevisiae
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Pred. No. 19;
3; Mismatches
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Pred. No. 21;
3; Mismatches
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R;Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54582
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  536 DIDIGVNTIKSDPDGVTVDD
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| 199 NTTTGLYGLKTE 210
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Best Local Similarity
Matches 8; Conserva
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Best Local Similarity
Matches 7; Conserv
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A;Molecule type: DNA
A;Residues: 1-584 <SC1
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1. Bacteriol. 183, 4833, 4838, 2001
A.Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A.Reference, number: A96900; MUID:21359325; PMID:21359325
R;Xu, J.C.; Lytle, C.; Zhu, T.T.; Payne, J.A.; Benz Jr., E.; Forbush III, B.
Proc. Natl. Acad. Sci... S.A. 31, 2201-2205, 1994 ...
A.Title: Molecular. Cloning and functional expression of the bumetanide-sensitive Na-K-Cl
A;Reference number: A53491; MUID:94181560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: JE0221.
Reddy, G.R.; Sulsona. C.R.; Barbet, A.F.; Mahan, S.M.; Burridge, M.J.; Alleman, A.R. Lochem. Blophys. Res. Commun. 247, 636-643, 1998
Title: Molecular characterization of a 28kba surface antigen gene family of the tribe. Reference. number: JE0216; MUID:98321180
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A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-133 <RED>
A;cross-references: GB:AF062762; NID:93327964; RIDN:AAC26722.1; PID:93327966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Ehrlichia canis
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Jul-2000
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                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1191 <XUA>
A;Cross-references: GB:U05958; NID:g454096; PIDN:AAB60617.1; PID:g454097
C;Superfamily: rat bumetanide-sensitive Na+/K+/C1--cotransport protein
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Pred. No. 2;
3; Mismatches
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Pred. No. 11;
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56.2%;

Query Match
Best Local Similarity 56.2
Matches 9: Conservative

13

RESULT

Mismatches Pred. No.

Conservative

Best Local Similarity Matches 10; Conserv

Query Match

Residues: 1-634 <KUR> Status: preliminary

A; Gene: CAC2212

Accession: F97172

C; Accession: F97172

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RESULT

a.

1 NTTTGVFGLKQDWDGATIKD 20

44.5%;

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Gaps ö

Length 160; Indels

A;Status: preliminary

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A,Cross.references: GB.AE001940; GB.AE000513; NID:g6458577; PIDN:AAF10437.1; PID:g645.A; Experimental source: strain R1 c.genetics:
C; Genetics:
A; Gene: DR0859
A; Map position: 1
C; Keywords: methyltransferase
                                                                                                                                                                                                                                                                                                                                           Mismatches
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Best Local Similarity 50...
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A; Residues: 1-160 <WHI>
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C:Accession: A75466
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M. S., Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                           R.Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Adaure 406, 959-964, 2000
A.Mature 406, 959-964, 2000
A.Mitle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patholy. A. Reference number: AB2950; MUID: 20437337
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1;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB06982.1; GSPDB:GN00
1;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira noteic Acids Res. 28, 4317-4331, 2000
Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and Reference number: A83650; MUID: 20512582; PMID:11058132
                                                                                                                                                                                                                                                                                                                                                                        n, meanucs: 1-40/ <210>
A;Cross-references: GB:AE004746; GB:AE004091; NID:g9949350; PIDN:AAG06627.1; GSPDB:GN001
A;Experimental source: strain PA01
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onserved hypothetical protein PA3239.[imported] - Pseudomonas aeruginosa (strain PAO1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0 1 · A 11
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Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
                                                             Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Bacillus halodurans
Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ypothetical protein BH3263 [imported] - Bacillus halodurans (strain C-125)
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Pred. No. 13;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46.5;
Pred. No. 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.3%;
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Best Local Similarity 77.8%;
Matches 7; Conservative
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Les 11; Conservative
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A;Gene: PA3239
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Matches
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 7, 2002; 14:30:38 ; Search time 10.34 Seconds (without alignments) 74.893 Million cell updates/sec Run on:

US-10-054-647-2

110 1 NTTTGVFGLKQDWDGATIKD 20 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapext 0.5 Gapext 0.5

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database:: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P55013 squalus aca	Q03263 saccharomyc	_			P37197 escherichia	P11129 bacteriopha					P39409 escherichia	032960 mycobacteri				Q9jvp2 neisseria m	_				7 escher:	P79775 gallus gall	zymomoi	7	377	~	~	80		5302 1	7361	O32106 bacillus su
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QI	NKC1_SQUAC	YM8M_YEAST	MENG_DEIRA	K6PF_CAEEL	YOAK_BACSU	YHJA_ECOLI	VP3_BPPH6	ATIA ARTSF	AROE SYNY3	PYRC_BACCL	A1A1_CANFA	YJJW_ECOLI	YM16_MYCLE	DNAA_STRCO	A1A2_HUMAN	GCST_NEIMB	GCST_NEIMA	YA67_METTH	KIME RAT	HTPG_PORGI			ANF1_CHICK	PURL_ZYMMO	DPYD_HUMAN	GVM1_HALN1	YRAJ_BACSU	PGHD_URSAR	BIOB_HELPJ	BIOB_HELPY	Y33B_MYCPN	- 1	AMPA_BACSU
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P31627 caprine art P06686 rattus norv P05023 home sapien P13607 drosophila P55012 mus musculu P55011 home sapien P13508 caenorhabdi P14585 caenorhabdi P24620 micromonosp P40756 rana, catesb Q97912 clostridium P24021 aspergillus	
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ENV_CAEVG A1A2_RAT A1A1_HUANA A1NA_UNCNE NKC1_HUAN GLP1_CAEEL L112_CAEEL YGRM_MICEC ANFD_RANCA ANFD_RANCA ANFD_CICAB UTD_CICAB UTD_CICAB UTD_CICAB UTD_CICAB	
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942 1020 1020 1021 1205 1212 1295 1429 1189 267	
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# ALIGNMENTS

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Gaps

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Indels

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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Probable S-adenosylmethionine:2-demethylmenaquinone methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    radiodurans R1.";
Science 286:1571-1577(1999).
-!- FUNCTION: CONVERTS DIMETHYLMENAQUINONE (DMK) TO MENAQUINONE (MK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Wakacova K.S., Azavind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus NCBL_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                             Length 540;
                                                                                                                         687D06CB0D70AF91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity).
-!- PATHWAY: LAST STEP IN MENAQUINONE BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE MENG FAMILY.
                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.9%; Score 45; DB 1
50.0%; Pred. No. 2.5;
iive 3; Mismatches
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                                                                                                                                                               Score 47;
Pred. No.
                                    POTENTIAL. POTENTIAL.
                                                                         POTENTIAL.
POTENTIAL.
                      POTENTIAL
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01-MAR-2002 (Rel. 41, Last seg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE001940; AAF10437.1; -
                                                                                                                           59561 MW;
                                                                                                                                                             42.7%;
                                                                                                                                                                                                                                256 NVPTNIHGLSMDWTGSAL 273
                                                                                                                                                                                                                1 NTTTGVFGLKQDWDGATI 18
                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                            Deinococcus radiodurans
                                                                                                                         540 AA;
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nes 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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Q9RW10;
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MENG_DEIRA
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                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
--- SIMILARITY: BELONGS TO THE MAJOR FACILITATOR FAMILY (ALSO KNOWN AS THE DRUG RESISTANCE TRANSLOCASE FAMILY). DHAIZ SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                            (POTENTIAL) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Hypothetical 59.6 kDa protein in DSK2-CAT8 intergenic region.
                                                                                                                                                                                                                                                                                                                                 Score 51, DB 1; Length 1191;
pred. No. 2.2;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                            BA7BB9815431500C CRC64;
                                                                                                               EXTRACELLULAR (POTENTIAL).
                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pearson D., Bowman S., Barrell B.G., Rajandream M.A.;
                                                                                     CYTOPLASMIC (POTENTIAL). POTENTIAL.
  CYTOPLASMIC (POTENTIAL).
                                    POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
POLY-PRO.
                                                                                                                                                                                                                                                        GLCNAC.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     856 TLVFGFKKDWRQALMKD 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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796
1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-S288C / AB972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MR279C OR YM8021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
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                                                                  rmatics Institute. There are no restrictions on institutions as long as its content is in no
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                                                                                                                                  Usage by and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medigue C., Moszer I., Viari A., Danchin A.; "Analysis of a Bacilius subtilis genome fragment using a co-operative computer system prototype."; Gene 165:GC37-GC51(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.L., Plunkett G. III, Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                       Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S., Sato T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94316500; PubMed-8041620;
Sofia H.J., Burland W., Daniels D.L., Plunkett G. III, Blattner F.
Sofia H.J., Burland W., Daniels D.L., Plunkett G. III, Blattner F.
Analysis of the Escherichia coli genome. V. DNA sequence of the region from 76.0 to 81.5 minutes.";
Nucleic Acids Res. 22.2576-2586(1994):
-i-CAPALITIC ACTIVITY: 2 ferrocytochrome c + H(2)0(2) = 2
ferricytochrome c + 2 H(2)D.
-i-PTW: BINDS 3 HEMES (POTENTIAL).
-i-SIMILARITY: HIGH, TO P. AERUGINOSA CYTOCHROME C551 PEROXIDASE.
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Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                           Y.;
DNA
                                                                                              Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi "Complete nucleotide sequence of a skin element exclsed by rearrangement during sporulation in Bacillus subtilis."; Microbiology 141:323-327(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 1; Length 284;
Pred, No. 6.7;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 protein; Complete proteome.
284 AA; 32170 MW; F255261D4692ADB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ol-ocr-1994 (Rel. 30, Last sequence update)
16-0cr-2001 (Rel. 40, Last annotation update)
Probable cytochrome C peroxidase (EC 1.11.1.5)
YHJA OR B3518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  465 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96084975; PubMed-7489895;
                SEQUENCE FROM N.A.
STRAIN-168 / JH642;
MEDLINE-95219086; Pubmed-7704261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last seq
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D32216; BAA06925.1; 1-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAB14569.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SubtiList; BG11262; yqaK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 FGWKNDWDAMALK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 7 FGLKQDWDGATIK 19
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-168 / JH642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 299117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical
SEQUENCE 26
                                                                                                                                                                                                                                                                                                                                                           Takeuchi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YHJA_ECOLI
P37197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YHJA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
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                   SOW REPAYED BY REPAYED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update).
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 32:2 kDa protein in SPOIIIC-CWLA intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last amotation update)
Probable 6-phosphofructokinase (EC 2.7.1.11) (Phosphofructokinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS: PRO0476; PHPRCTKINASE.
ProDom: PD000707; Phosphofructokinase; 2.
PRGSITE; PS00433; PHOSPHOFRUCTOKINASE; 1.
Kinase; Transferase; Glycolygis: Repeat.
SEQUENCE 756 AA; 83301 MW; 26A89B801D286534 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Firmicutes: Bacillus/Clostridium group;
Bacillus/Staphyldcoccus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
40.9%; Score 45; DB 1;
Best Local Similarity 53.3%; Pred. No. 13;...
Matches 8; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WormPep; C50F4.2; CE05467.
INterPro; IPR000023; Phosphofructokinase.
Pfam; PF00365; PFK; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z70750; CAA94737.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         436 VIGIKHGWDGLKNKD 450
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFGLKQDWDGATIKD 20
GVFGLKQDWDGATI 18
                                             (Phosphohexokinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YQAK_BACSU
P45908;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McMurray A.;
                                                                                                                                                                                                                                K6PF_CAEEL
                                                                                                                                                               RESULT
K6PF_CAREL
AC 027483
DT 15-JUL
DT 15-JUL
DE (Phosp)
GN CSOF4;
OC ENARY
OC RABDIL
ON (11)
RP SEQUEN
RA MCMULTI
RL SUBMIT
CC 1- PR
CC 1- PR
CC 1- PR
CC 1- PR
CC 1- CA
CC 1- PR
CC
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YQAK_BACSU
AC P45908,
DT 01-NOV
DT 16-OCT
DE HYPOTH
GN YQAK:
OS BACILI
OC BACILI
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                      the European Bioinformatics Institute. There are no restrictions on its use by, non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
       and the EMBL outstation
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1 (HEME PROXIMAL) (BY SIMILARITY).
2 (COVALENT) (BY SIMILARITY).
2 (HEME PROXIMAL) (BY SIMILARITY).
3 (COVALENT) (BY SIMILARITY).
3 (COVALENT) (BY SIMILARITY).
4 (COVALENT) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HEME PROXIMAL) (BY SIMILARITY). (HEME DISTAL) (BY SIMILARITY). A698949E6DA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44; DB 1; Length 465; pred. No. 11; 4; Mismatches 2; Indels
                                                                                                                                                                                                            Ecodene; EG12244; yhjA.
InterPro; IPR000345; CytC_heme_bind.
InterPro; IPR00345; CytC_teme_bind.
InterPro; IPR00345; CytCot.
Pfam; PF00034; CytCothcome.c. 1.
PROSITE; PS00190; CYTCOTHROME.C; 3.
Hypothetical protein; Oxidoreductase; Peroxidase; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69178 MW; B188DFE02ACC54E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses, dsRNA, viruses, Cystoviridae, Cystovirus NCBI_TaxiD-10879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9F494A698949E6DA
between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                         lectron transport; Complete proteome. ...
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11, Last sequence update)
13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          648 AA
                                                                                                                                                                                                                                                                                                                                                                                                        HEME 1
IRON 1
HEME 2
IRON 2
IRON 2
HEME 3
IRON 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                             EMBL;, AE000428; AAC76543.1; -.
                                                                                                                                                                       EMBL; U00039; AAB18494.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M17462; AAA68485.1; -. PIR; C28648; P3BPF6. Envelope proteinf SEQUENCE 648 AA; 69178 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFGLKQDWDG--ATIKD 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              210
210
211
211
35
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01-JUL-1989 (Rel. 11,
01-JAN-1990 (Rel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacterlophage phi-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P3 protein.
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Р11129;
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Best Local S
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SEQUENCE
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BINDING
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAL .
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AC O1-JU
DT O1-JU
DT
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Ö
                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sodium/potassium-transporting ATPase alpha chain (EC 3.6.3.9) (Sodium
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDINEd-1657719; MEDLINE-92039032; PubMed-1657719; MACIAE M.Y., MATLINE-2039032; MACIAE M.Y., MATLINEZ J.L., Palmero I., Sastre L.; "Cloning of a cDNA encoding an Artemia franciscana Na/K ATPase alpha-
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                            pump) (Na+/K+ ATPase).
Artemia sanfranciscana (Brine shrimp) (Artemia franciscana).
Eukaryota, Metazoa; Arthropoda; Crustacea; Branchiopoda; Anostraca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 ATPASES). SUBFAMILY IIC.
                              ..
73
 Length 648
                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00122; E1-E2_ATPase; 1.
Pfam; PF00702; Hydrolase; 1.
PRINTS; PR00119; CATATPASE.
PRINTS; PR00121; NAKATPASE.
PROSITE; PS00124; APPASE_E1_E2; 1.
Hydrolase; Sodium/potassium transport; Transmembrane;
DB 1;
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                            PRT; 1004 AA
                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
    Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR004014; Catlon_ATPase.
Interpro; IPR001757; E1-E2_ATPase.
Interpro; IPR001454; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00689; Cation_ATPase_C; 1. Pfam; PF00690; Cation_ATPase_N; 1.
                                                                                                                                                                                            01-DEC-1992 (Rel. 24, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hosphórylation; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X56650; CAA39972.1; -.
    40.0%;
                                                                                       181 IFGWYVKMDWEGSAVAD 197
                                                            6 VFG--LKQDWDGATIKD 20
      Query Match
Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                               STANDARD;
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HSSP; P04191; 1EUL.
                                                                                                                                                                                                                                                                                              Artemiidae; Artemia
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND GAMMA.
                                                                                                                                                              AT1A_ARTSF
P28774;
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342 TGVFTLKOLVDWLTIK 357
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                                                                                                                               Bacillus caldolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                          SEQUENCE: FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEROPS; M38.972
                                                                                                                                                                                                                              STRAIN-DSM 405;
                                                                                                                                                                                                                                                                                                                                               aspartate.
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P50997;
                  PYRC_BACCL
P46538;
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                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL distraction the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions, as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensedsed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyalima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Sequence analysis of the genome of the genome of the genome of the genome and assignment of potential protein-coding regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- PATHWAY: FOURTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - CATALYTIC ACTIVITY: Shikimate + NADP(+) - 5-dehydroshikimate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 1; Length 1004;
pred No. 26; Length 1004;
                                                                                                                                                              5, Indels
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (PROBABLE).
                                                                              MW; CE4E6BECE19A78C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR002907; Shikimate_DH.
Pfam; PF01488; Shikimate_DH; 1.
Aromatic amino acid biosynthesis; Oxidoreductase; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
SEQUENCE 290"AA; 31099 MW; 8A2D38EE5D57B303 CRC64;
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                                                                                                                                                                                                                                                                                                    PRT 290 AA
                                                                  ATP (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                     P.(35);
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Shikimate 5-dehydrogenase (EC 1.1.1.25).
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Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-97061201; Pubmed-8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 TTTGVFG------LKQDWDGAT 17
                                                                              1004 AA; 110699
                                                                                                                            Query Match
Best Local Similarity 40.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                          AROE SYNY3 STANDARD)
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                                                                                                                                                                                            6 VFGLKQDWDGATIKD 20
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               TRANSMEM
TRANSMEM
MOD_RES
BINDING
SEQUENCE
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 TRANSMEM
                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-9428293; PubMed-7516791;
Ghim S.Y., Nielsen P., Neuhard J.;
"Molecular: characterization of pyrimidine biosynthesis genes from the
thermophile Bacillus caldolyticus.";
Microbiology 140:479-491(1994).
-1- CATALITIC ACTIVITY: (S)-dihydroorotate + H(2)0 = N-carbamoyl-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -: COPACTOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WHICH IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY TO TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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01-0CT-1996 (Rel. 34, Last sequence update),
16-0CT-2001 (Rel. 40, Last sequence update),
Sodium/potassium-transporting Afrase alpha-1 chain precursor
(EC 3.6.3.9) (Sodium pump 1) (Na+/K+ ATPase, 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- PATHWAY: THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO,THE DHOASE FAMILY. SUBFAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 1; Length 427;
Pred. No. 15;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      759A2AA99F733F4E CRC64;
                                                                                                                                                                                                      Bacteria, Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
NCBL_raxID=1394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC (POTENTIAL). ZINC (POTENTIAL).
                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-TOT-2001 (Rel. 40, Last annotation update)
Dihydroorotase (EC 3.5.2.3) (DHOase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1021 AA.
427 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pyrimidine blosynthesis; Hydrolase; Zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prosite; Pro0744; Dihydroorotase; 1: PROSITE; PSO0482; DIHYDROOROTASE_1; 1. PROSITE; PSO0483; DIHYDROOROTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002195; Dihydrooratase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL 62 62 Z
SEQUENCE 427 AA: 46047 MW;
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Best Local Similarity 68.8%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X73308; CAA51737.1; -
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RESULT

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YJJW_ECOLI
ID YJJW_ECOLI
AC P39409;
                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMED distraction the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.ch.)
                                                                                                                                                                                                                                                                                                                                                                       -1- FUNCTION: THIS IS THE CATALYTIC COMPONENT OF THE ACTIVE ENZYME, WHICH CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF WHICH CATALYZES THE PLASMA MEMBRANE. THIS ACTION CREATES THE ELECTROCHEMICAL GRADIENT OF 'NA AND K, PROVIDING THE ENERGY FOR ACTIVE TRANSPORT OF VARIOUS NUTRIENTS.
-1- CATALYTIC ACTIVITY: ATP + H(2)0 + Na(+)(in) + K(+)(out) - ADP + Phosphate + Na(+)(out) + K(+)(in).
-1- SUBUNIT: COMPOSED OF THREE SUBUNITS: ALPHA (CATALYTIC), BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00154; ATPASE E1 E2; 1.

Hydrolase; Sodium/potassium transport; Transmembrane; Phosphorylation; Magnesium; Metal-binding; ATP-binding; Multigene family.

1 5 BY SIMILARITY.

CHAIN 6 1021 SODIUM/POTASSIUM-TRANSPORTING ATPASE
                                                                                                                                                                                                                                                                 Canessa C.M., Horisberger.J.-D., Louvard.D., Rossier B.C.; "Mutation of a cysteine in the first transmembrane segment of Na.K-ATPase alpha subunit confers ouabain resistance."; EMBO J. 11:1681-1687(1992);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. SUBCELLUIAR LOCATION: Integral membrane protein,
1. SIMILARITY: BELONGS TO THE CATION, TRANSPORT ATPASES FAMILY (E1.E2 ATPASES). SUBFAMILY IIC.
                                                       XIG Z., Li H., Liu G., Wang Y., Askarl A., Mercer R.W.;
Cloning of the dog Na/K-Arbase alpha i subunit.";
(In) Bamberg E., Schoner W. (eds.);
The sodium pump, pp.49-52, Springer.Verlag, New York (1994);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALPHA-1 CHAIN.
CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                     TISSUE-Kidney;
MEDLINE-92258376; Pubmed-1316269;
                                                                                                                                                                                         SEQUENCE OF 92-307 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00119; CATATPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND GAMMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                               ö
PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY CAPK) (BY
                                                                           SIMILARITY).
BINDING OF PHOSPHOINOSITIDE-3 KINASE (BY BINDING OF SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                           Length 1021,
                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A..
STRALN-X12 / MG1655,
MEDLINE-95334362; Pubmed-7610040;
Burland V.D., Plunkett G. III, Sofia H.J., Danlels D.L.,
                                                                                                                                                                                                                                                                                                       MW; 938A19AA487CBEAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 1;
Pred. No. 39;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein yjjw.
                                                                                                                                                                                                      C -> Y (IN REF.
I -> V (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ECGGENE, EG1259; Y1W.
ECGGENE, EG1259; Y1W.
InterPro; IPR001450; 4Fe4S.ferredoxin.
InterPro; IPR001989; Radical_activat.
Ffam; PF00137; fer4; 2;
Ffam; PF02143; Radical_activat; 1.
ProDom; PD004758; Radical_activat; 1.
PROSITE; PS00198; 4FE4S.FERREDOXIN; 2.
PROSITE; PS01087; RADICAL_ACTIVATING; 1.
                                                                                                                                                                                                                                                        Ω <u>ω</u>
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000508; AAC77332.1;
HSSP; P00198; 2FDN:
                                                                                                                                                                                                                                                                                                         112666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TGVFGLKQDWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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9 LKQDWDGAII 18

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143 LCQDWEGATL 152
                                                                    RESULT 14
DNAA_STRCO
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                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Hondre N., Garnier T., Churcher C., Harris D., Mudgall K., Basham D., Strom D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthor, S., Rejtwell T., Fraser A., Hamlin N., Holtcyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Ollver K., Quail M.A., Rajandream M.A., Rutherford K.M., Stutter S., Seeger K., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                      (4FE-4S) (BY SIMILARITY)
(4FE-4S) (BY SIMILARITY)
(4FE-4S) (BY SIMILARITY)
                                                                                                                                     (BY SIMILARITY (BY SIMILARITY
                                                                                             SIMILARITY
Iron-sulfur; 4Fe-4S; Complete proteome.

IRON-SULFUR (4FE-4S) (BY SIMILARITY)
IRON-SULFUR (4FE-4S) (BY SIMILARITY)
IRON-SULFUR (4FE-4S) (BY SIMILARITY)
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                                                                                                                                                                                                 Query Match 38.2%; Score 42; DB 1; Length 287; Best Local Similarity 50.0%; Fred. No. 14; Matches 8; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 38.2%; Score 42; DB 1; Length 307; Best Local Similarity 70.0%; Pred. No. 16; Matches 7; Conservative 2; Mismatches 1; Indels
                                       IRON-SULEUR (4FE-4S) (BY SIM
IRON-SULEUR 1 (4FE-4S) (BY S.
IRON-SULEUR 2 (4FE-4S) (BY S.
IRON-SULEUR 2 (4FE-4S) (BY S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 11 May 1 1 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium leprae.
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae.
                                                                                                                                                   RON-SULFUR 2 (4FE-4S) (B)
E08BB429519E54B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome:
SEQUENCE 307 AA; 32853 MW; EEFESBA102455DA2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Massive gene decay in the leprosy bacillus.";
Nature 409:1007:1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ature 409:100/TIOI1(2001).
|- SIMILARITY: BELONGS TO THE UPF0105 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                         03.2300.
30.MAY-2000 (Rel. 39, Created)
30.MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 32.9 kDa protein ML0860.
                                                                                                                                                                                                                                                                                                                                                       PRT; 307 AA
                                                                                                                                                              31490 MW;
                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                   50
53
76
79
                                               AL583920; CAC31241.1;
                                                                                                                                                                                                                                                                        249 GVYGEAQSWASATPED 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; 298741; CAB11383.1;
                                                                                                                                                                                                                                                         5 GVFGLKODWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                                     ML0860 OR MLCB22,18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM .N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CBI_TaxID-1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leproma; ML0860;
    Hypothetical:
                                                                                                                                                                                                                                                                                                                         RESULT 13
YM16_MYCLE
ID YM16_MYCLE
AC 032960;
                                                                                                                                                              SEQUENCE
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METAL
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL FUNCTION: PLAYS'AN IMPORTANT, ROLE IN THE INTITATION AND REGULATION OF CHROMOSOMAL REPLICATION, BINDS, TO THE ORIGIN OF REPLICATION; IT BINDS, SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BP CONSENSUS (DNA BOX): 5'-TTATC(C/A)A(C/A)A; DNAA BINDS TO ATP AND TO ACIDIC PHOSPHOLIFIDS.

ACIDIC PHOSPHOLIFIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        "Conserved gene arrangement in the origin region of the Streptomyces coelicolor chromosome.";
                                                                                                                                                                            Streptomyces coelicolor.

Bacteria; Firmloutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-A3(2);
Brown S.P., Harris D., Cerdeno A.M., Parkhill J., Barrell B.G.,
Rajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FP (POTENTIAL).
6C1D5C0193D3C92B CRC64;
                    P27902; O9KXX4;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Chromosomal replication initiator protein dnaA.
DNAA OR, SCH18:16C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.2%; Score 42; DB 1; 36.8%; Pred. No. 35; ative 5; Mismatches
656 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1020 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA replication; DNA-binding; ATP-binding NP_BIND 357 364 ATP (POTENTI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb_sib.ch)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriol. 174:3220-3226(1992);
                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2);
MEDLINE-92250416; Pubmed-1577691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 51-656 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 .364 A
656 AA; 73182 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A41870; A41870.
Interpro; IPR003593; AAA.
Interpro; IPR001957; Bac_DnaA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF187159; AAA26734.1; -. EMBL; AL357152; CAB92999.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 TSTAIMGATADYFGLTVED 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 TITGVFGLKODWDGATIKD 20
                                                                                                                                                                                                                                                                                                                                                                                                                     Calcutt M.J., Schmidt F.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 36.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROSITE; PS01008; DNAA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00308; bac_dnaA;
PRINTS; PR00051; DNAA.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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ID Ala2_HUMAN
DNAA_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDUAGOUS N.N.;
"Family of human Na+,K+-Arpase genes. Structure of the putative
regulatory region of the alpha+-gene.";
FEBS.Lett. 24.481-483[1989].

-!- FERS.Lett. 24.481-483[1989].

-!- FUNCTION: THIS IS THE CATALITIC COMPONENT OF THE ACTIVE ENZYME,

-!- FUNCTION: THIS IS THE PLASMA MEMBRANE. THIS ACTION CREATES THE
ELECTROCHEMICAL GRADIENT OF NA AND K, PROVIDING THE ENERGY FOR
ACTIVE TRANSPORT OF VARIOUS NUTRIENTS.

-!- CATALITIC ACTIVITY: ATP + H(1)(10) + K(+)(out) = ADP.+

phosphate + Na(+)(out) + K(+)(in).

-!- SUBUNIT: COMPOSED OF THREE SUBUNITS: ALPHA (CATALITIC), BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hull M.M., Lingrel J.B.; Multiple genes encode the human Na+,K+-ATPase catalytic subunit."; multiple genes encode the human Na+,K+-ATPase catalytic subunit."; roc. Natl. Acad. Sci. U.S.A., 84:4039-4043(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ostina M.B., Sverdlov V.E., Modyanov N.N., Ovchnikov Y.A.; The family of human Na+ K+. -ATPase genes: No less than five genes nd/or pseudogenes related to the alpha-subunit.";
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-4 FROM N.A.
MEDLINE-89153603; PubMed-2537767;
SYSTÉGIOW E.D., BESSATAD D.A., MALYSHEV I.V., PETRUKHIN K.E.,
SMITHOV Y.V., USHKATYOV Y.A., MONASTYTSKAYA G.S., Broude N.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLUIAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IIC.
                 01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last.sequence.update)
16-OCT-2001 (Rel. 40, Last.annotation.update)
Sodium/potassium-transporting Arpsase alpha-2 chain precursor (EC 3.6.3.9) (Sodium pump 2) (Na+/K+ Arpsase 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Placenta, and Brain;
MEDLINE-87247232; PubMed-3036582;
Sverdlov E.D., Monastyrskaya G.S., Broude N.E., Ushkaryov Y.Sverdlov E.D., Melkov A.M., Smirnov Y.V., Malyshev I.V., Dulobova I.E., Petrukhin K.E., Grishin A.V., Kijatkin N.I., Rostina M.B., Sverdlov V.E., Modyanov N.N., Ovchnikov Y.A.;
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-90008924; PubMed-2477373;
Shull M.M., Pugh D.G., Lingrel.J.B.;
Characterization of the human Na,K-ATPage alpha 2 gene and identification of intragenic restriction fragment length polymorphisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDLINE-87231946; PubMed-3035563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M27571; AAA35575.1; JOINED.
EMBL; M27576; AAA95575.1; JOINED.
EMBL; Y07494; CAA68793.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE OF 211-249 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J05096; AAA51797.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQUENCE OF 251-442 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nd/or pseudogenes related to EBS Lett. 217:275-278(1987).
                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                            ISSUE-Leukocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M27576; P
P50993; 007059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fodyanov N.N.;
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Interpro; IPR001454; Hydrolase.
Interpro; IPR001454; Hydrolase.
Interpro; IPR000661; Na.H.K.ATPase.
Pfam; PF00690; Cation_ATPase_C; 1.
Pfam; PF00102; E1-E2_ATPase; 1.
Pfam; PF00102; Hydrolase; 1.
PRINTS; PR00119; CATATPASE; PR0118; PR00119; NAKATPASE; PR051TE; PS00154; ATPASE_E1_E2; 1.
PROSTTE; PS00164; ATPASE_E1_E2; 1.
PROSTE; PS00104; ATPASE_E1_E2; 1.
PROSPEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING OF PHOSPHOINOSITIDE-3 KINASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                   SODIUM/POTASSIUM-TRANSPORTING ATPASE
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PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY CAPK) (BY
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Pred. No. 57;
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MAGNESIUM (BY SIMILARITY).
M; AFBD8EA94FFB4FC3 CRC64;
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CYTOPLASMIC (POTENTIAL)
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1020 AA; 112265
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Best Local Similarity 40.0%;
Matches 6; Conservative
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HSSP; PO4191; 1EUL.
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., Broude N.E., Ushkaryov Y.A.,

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7, 2002, 14:33:58 Search completed: June Job time:, 200 sec

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June 7, 2002, 14:30:18; Search time 25.04 Seconds (without alignments) 138.175 Million cell updates/sec
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GenCore version 4.5,
Copyright (c), 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                           562222 seqs, 172994929 residues
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                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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<u>a</u>	Q92GJ2 PRELIMINARY; PRT; 288 AA.
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DŢ	(TrEMBLrel. 10,
百	(TrEMBLrel. 17,
OE	30-KDA MAJOR OUTER MEMBRANE PROTEIN (P28-8).
N S	P30 OR P28-8.
SO	Ehrlichia canis.
8	Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
8	
ŏ	NCBI_TaxID=944;
N.	[1]
ЯP	SEQUENCE FROM N.A.
RC	STRAIN-OKLAHOMA; ''.
RX	MEDLINE-98371112; Pubmed-9705412;
RA	Ohashi N., Unver A., Zhi N., Rikihisa Y.;
RT	"Cloning and characterization of multigenes encoding the
RŢ	immunodominant 30-kilodalton major outer membrane proteins of
RT	Ehrlichia canis and application of the recombinant protein for
RI	serodiagnosis.";
몺	J. Clin. Microbiol. 36:2671-2680(1998).
RN	[2]
ЯP	SEQUENCE FROM N.A.
RC C	STRAIN-JAKE;
RX	MEDLINE-99242757; PubMed-10225842;
RA	
RT	a conserv
RI	28-kilodalton protein of Ehrlichia canis: a potential serodiagnostic
RT	
Æ	Clin. Diagn. Lab. Immunol. 6:392-399(1999).
RN	[8]
RP	SEQUENCE FROM N.A.
2	STRAIN-JAKE;
RX	MEDLINE~20432107; PubMed~10974556;
RA	McBride J.W., Yu X.J., Walker D.H.;
RT	"A conserved, transcriptionally active p28 multigene locus of
RT	Ehrlichia canis.";

Gaps

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Molecular characterization of a 28 kDa surface antigen gene family of
                                                                                                         Reddy G.R., Sulsona C.R., Barbet A.F., Mahan S.M., Burridge M.J.,
Alleman A.R.;
                                                                                                                                                                                                                                                                                                                                                                                   Score 90; DB 2; Length 280;
Pred: No. 5e-06;
                                                                                                                                                                                           the tribe Ehrlichiae.";
Blochem. Blophys. Res: Commun. 247:636-643(1998).
EMBL. AF062761.1;
InterPro. IPR002566; Surface.Ag_msp4.
Pfam: PF01617; Surface.Ag_2: 1.
SEQUENCE 280 AA; 30743 MW; FBB841DAF08EE4DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                       STRAIN-ARKANSAS;
MEDLINE-98321180; PubMed-9647746;
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NON_TER 1 1
SEQUENCE 246 AA; 26884 MW;
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Best Local Similarity 88.9%;
Matches 16; Conservative
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Best Local Similarity 83.3
Matches 15; Conservative
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093004;
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Matches
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                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohashi N., Rikihisa Y., Unver A.;
Analysis of Transcriptionally Active Gene Clusters of Major Outer
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                                                                                                                                                                                           Query Match
100.0%; 'Score 110', DB 2; Length 288;
Best Local Similarity 100.0%; Pred. No. 4.1e-09;
Matches 20; Conservative 0; Mismatches 0; Indels '
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Rickettsiaceae; chrlichieae; Ehrlichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rickettslales;
Rickettslaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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280 Aa; 30731 MW; CCAA6C34E2AF393E CRC64;
                                                                                                    Pfam; PF01617; Surface_Ag_2; 1...
SEQUENCE 288 AA; 31590 MW; 86DCAECB88E9BF5E CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
28 KDA MAJOR SURFACE ANTIGEN-4.
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Last annotation update)
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EMBL, U72291; AAC02940.1; -.
InterPro; IPR002566; Surface_Ag_msp4.
                                                                    PR002566; Surface_Ag_msp4.
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                          EMBL; AF078553; AAC68607.1;
EMBL; AF082744; AAG14362.1
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Yu X.J., McBride J.W., Walker D.H.,
"Genetic diversity of the 28-kilodalton outer membrane protein gene in
human isolates of Ehrlichia chaffeensis.";
J. Clin. Microbiol. 37:1137-1143(1999).
EMBL: AF077735; AAC31548.1;
Interpro; IPR001702; Gram.neg_porin.
Interpro; IPR002566; Surface_Ag_msp4.
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Ehrlichia chaffeensis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                    Ehrlichia chaffeensis.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13} Last sequen
01-DEC-2001 (TrEMBLrel. 19, Last annots
OUTER MEMBRANE PROTEIN P28 (FRAGMENT)
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01-DEC-2001 (TrEMBLrel: 19, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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MEDLINE-99175287; Pubmed-10074538;
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SORETERS

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"Molecular characterization of a 28 kDa surface antigen gene family of
the tribe Ehrlichiae.";
Biochem. Biophys. Res. Commun. 247:636-643(1998).
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                                                                                                                                                                                                                                                 Long S.W., Zhang X.-F., Q1 H., Standaert S., Walker D.H., Yu X.-J
"Allele variation and patterns of transcription of the Ehrlichla
Chaffeensis 28 Nob" outer membrane. protein multigene family.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF393393; AAL12923.1;
SEQUENCE 276 AA; 30028 MW; 2D7143AFCBFFZEBE CRC64;
                                                                                                     Ehrlichia chaffeensis:
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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01-DEC-2001 (TrEMBLrel. 19, Created)
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00TER MEMBRANE PROTEIN P28.
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Best Local Similarity 83.3%; Pred. No. 2.1e-05;
Matches 15; Conservative 1; Mismatches 2;
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InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
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MEDLINE-98321180; Pubmed-9647746;
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'Genetic diversity of the 28-kilodalton outer membrane protein gene in
htwan isolates of Ehritchia chaffeensis.";
J. Clin. Microbiol. 37:1137-1143(1999).
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EMBL; AR93335; AAL12925.1; -Interpro; IPR002566; Surface_Ag_msp4.

Pfam; PF01617; Surface_Ag_msp4.

SEQUENCE 276, AA; 30027, WW; ZFD3698FCFIF60BE CRC64;
                                                                                                 Jaralna V. 2. Jang X.-F., Ql. H., Standaert, S., Walker D. H., Yu X.-J., Long S. W. 2. Annual variation and patterns of transcription of the Ehrlichia chaffeensis 28 kDa outer.membrane protein multigene family "; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
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Rickettsiaceae, Ehrlichieae, Ehrlichia.
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Best Local Similarity 83.3%; Pred. No. 2.1e-05;
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
00TER MEMBRANE, PROTEIN P28.
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Rickettslaceae; Ehrlichieae; Ehrlichia.
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MEDLINE-99175287; PubMed-10074538;
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                                                         SEQUENCE FROM 'N.A.
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Yu X.J., MCBride J.W., Walker D.H.; "Genetic diversity of the 28-kilodalton outer membrane protein gene in human isolates of Ehrlichia chaffeensis.";
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MEDLINE-99175287; PubMed-10074538;

Yu X.J., McBride J.W., Walker D.H.;

Genetic diversity of the 28-kilodalton outer membrane protein gene in human isolates of Ehrlichia chaffeensis.";

J. Clin. Microbiol. 37:1137-1143(1999).
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Bacteria; Proteobacteria; alpha subdivision; Rickettslales;
Rickettslaceae; Ehrlichieae; Ehrlichia.
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Rickettsiaceae; Ehrlichieae; Ehrlichia
NCBI_TaxID=945;
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Pred, No. 0.00012;
2; Mismatches 2; Indels
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Yu X.-J., Walker D.H.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF077733; AAC31546.1} ...
InterPro; IPR002566; Surface_Ag_msp4.
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SEQUENCE 280 AA; 30304 MW; 91C54AC7851B77F2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19; Last annotation update)
00TER MEBBRANE PROTEIN P28.
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Local Similarity 77.8%;
nes 14; Conservative
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                   59 NTTVGVFGLKQNWDGSAISN 78
NTTIGVEGLKQDWDGATIKD 20
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Obashi N., Zhi N., Zhang Y., Rikihisa Y.;
Immunodominant major outer membrane proteins of Ehrlichia chaffeensis
are encoded by a polymorphic multigene family.";
Infect. Immun. 66:132-139(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S., Walker D.H., Yu X.-J.;
                                                                                                                                                                                                                                                                                                                               Ohashi N., Rikihisa Y., Unver A.; "Analysis of Transcriptionally Active Gene Clusters of Wajor Outer Membrane Protein Multigene Family in Ehrlichia canis and E. chaffeensis.";
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Bacteria; Proteobacteria: alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
                                         Ehrlichia chaffeensis.
Bacteria: Proteobacteria: alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
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70.0%; Pred. No. 8.7e-05; Undels
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Interpro; IPRO02566, Surface_Ag_msp4.
Pfam; PF01617; Surface_22, 1. AS99E5F7C4459AA9A CRC64;
SEQUENCE 281 AA, 30343 MW, A999E5F7C4459AA9A CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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STRAIN-ARKANSAS;
MEDLINE-21153566; Pubmed-11254561;
       MAJOR OUTER MEMBRANE PROTEIN P28
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MEDLINE-21153566; PubMed-11254561;
Mohashi N., Rikhibas Y., Onver A.;
"Analysis of Transcriptionally Active Gene Clusters of Major Outer
Membrane Protein Multigene Family in Ehrlichia canis and E.
Ehrlichia canis and application of the recombinant protein for serodiagnosis.";
                                                                                                                                                                                                                                                                                                                                                                                         Length 280;
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InterPro; IPR002566; Surface_Ag_msp4.
Pfam; PF01617; Surface_Ag_2; 1.
SEQUENCE 280 Aa; 30803 MW; 27238BE1C7E68A91 CRC64;
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65.0%; Pred. No. 0.00052;
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                                                        r. Clin. Microbiol. 36:2671-2680(1998).
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MEDLINE-99242757; PubMed-10225842;
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EM&L: AF393391; AAL12921.1; -. SEQUENCE 280 AA; 30372 MW; C7BBC8710BC167E9 CRC64;
             Long S.W., Zhang X.-F., Q1 H., Standaert S., Walker D.H., Yu X.-J. "Allele variation and patterns of transcription of the Ehrlichia chaffeensis 28 KDa outer membrane protein multigene family."; Submitted (JMD-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF077732: AAC31545.1;
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MEDLINE-98371112, PubMed-9705412;
MEDLINE-9837112, Din N., Rikihisa Y.;
"Cloning and characterization of multigenes encoding the Immunodominant 30-kilodalton major outer membrane proteins of
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Rickettsiaceae; Ehrlichieae; Ehrlichia.
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EMBL; AF393390; AAL12920.1; -.
InterPro; IPR002566; Surface_Ag_msp4.
Pfan; PF01617; Surface_Ag_2; 1.
SEQUENCE 280 AA, 30277 MW, 91C54AC78507A63F CRC64;
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Pred. No. 0.00012;
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MAJOR OUTER MEMBRANE PROTEIN P30-2.
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MCBride J.W., Yu X.J., Walker D.H.;
McBride J.W., Yu X.J., Walker D.H.;
"A conserved, transcriptionally active p28 multigene locus of Ehrlichia canis.";
Ehrlichia canis.";
EMBL; AF082744; AAG14361.1; -.
InterPro; IPR002566; Surface_Ag_msp4.
                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rickettslales;
Rickettslaceae; Ehrlichleae; Ehrlichia.
NCBL_TaxID=944;
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